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Title:
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Listing first 45 summaries
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1: geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match

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	coding sequences of a r. These sequences can be in the treatment and rs including dermatitis, asthma and bronchitis.	nd inflammatory disorders, such	Sugimoro i, oca i;	!				gy;						Abull904 Human cys	Human	Human A huma	m o		Pig Li	Abul1962 Human HGP Abul1963 Human HGP	Aab85097 Truncated		Abull939 Human G-p	Aae08553 Human G-p Aae07539 Human G-p	

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08-FEB-2000;

09-FEB-2000;

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09-FEB-2000;

17-FEB-2000;

20-UUL-2000;
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                                                                                                                                                                                                                                                                                          08-FEB-2001;
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/label= Mature_human_GPCR1a_protein_variant
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/label= Signal_peptide
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Best Local Sim
Matches 346;
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Casman S, E
Mezes PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPCRX sequences are used to treat or prevent a human suffering from GPCR -associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosis, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematopoietic disorders useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful treating or preventing, e.g., cardiomyopathy, atherosclerosis, hypertension, acquired immune deficiency syndrome, bronchial ast Crohn's disease, and multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                          activity. This substance is useful for treating a subject having a disorder which is responsive to cysteinyl leukotriene receptor modulation, such as asthma, chronic obstructive pulmonary disease (COPD) allergic rhinitis, cardiac arrhythmia, myocardial ischaemia, atherosclerosis and heart failure. It is also useful in the therapeutic treatment and/or prophylaxis of discorders such as acquired immune deficiency syndrome (AIDS), rheumatoid arthritis, multiple sclerosis, leukaemia, myasthenia gravis, Grave's disease, systemic lupus erythematosus, inflammatory bowel disease, encephalomyelitis, psoriasis, erythematosus, inflammatory bowel disease, encephalomyelitis, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cysteinyl leukotriene receptor; HIPHUM0000007; antiasthmatic; antiHIV; antiallergic; antiinflammatory; antiarteriosclerotic; antiarthritic; vasotropic; cytostatic; neuroprotective; antixheumatoid; antiarthritic; immunosuppressive; antipsoriatic; dermatological; antibacterial; cerebroprotective; antithyroid; asthma; allergic rhinitis; AIDS; cardiac arrhythmia; myocardial ischaemia; atheroselerosis; heart failure; rheumatoid arthritis; immune disorder; dermatitis; septic shock; stroke.
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                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GPCR) that has 7 transmembrane regions. Homology searches showed this receptor to be homologous to cysteinyl leukotriene (cycLT1 LTD4) receptor and P2Y receptors. The invention provides P2Y-like GPCR polypeptides and polynucleotides, expression vectors, host cells, methods for detecting the polynucleotides, methods of screening for agents which regulate or decrease the activity of a P2Y-like GPCR protein, and a pharmaceutical
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                                                         Human; G-protein coupled receptor; GPCR; hRUP14; agonist;
inverse agonist; lung cancer.
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                                                                                                                                                                                                                                                                                                                                 NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                                                                                                                                                                                                                                                                                                                                                                           SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MERKFMSLOPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                       (first entry)
                                                                                                                 coupled receptor, hRUP14
                                                                                                                                                                                                                                   protein;
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Pred. No. 2.7e-180;
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Best Local
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23-DEC-1999
23-DEC-1999
11-FEB-2000
14-WAR-2000
10-APR-2000
10-APR-2000
10-APR-2000
110-APR-2000
28-APR-2000
28-APR-2000
28-APR-2000
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12-JUN-2000;
21-AUG-2000;
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17-NOV-1999;
17-NOV-1999;
                                                                                                                                                                                                                                                                                               The sequence represents a human G-protein coupled receptor (GPCR), hRUP14: The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-355616/37.
N-PSDB; AAS07941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; Page 100-101; 160pp; English.
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                                                                                                                                                                                    Similarity
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NGSVTSCLELNLYKIAKLQTMYYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                                                                                                                        MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
                                                          NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                            NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                                                                  YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
                                                                                                                                                        MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
                                                                                                                 YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
                                                                                                                                                                                                                                                                      346 AA;
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2000US-0189258P.
2000US-0189259P.
2000US-0195898P.
2000US-0195899P.
2000US-01960789.
2000US-0200419P.
2000US-0200419P.
2000US-0210741P.
2000US-0210741P.
2000US-0210741P.
2000US-0210741P.
                                                                                                                                                                                                             100.0%; Score 1788; DB 4; ilarity 100.0%; Pred. No. 2.7e-180; Conservative 0; Mismatches 0;
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2000US-0242343P.
2000US-0243019P.
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2000US-0235779P.
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ARESULT 6
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06-APR-2000; 2000US-0195155P.
20-APR-2000; 2000US-0199084P.
28-APR-2000; 2000US-0200551P.
05-MAY-2000; 2000US-0202278P.
The present sequence is a human G-proprotein. The GCRECs are used for treasesciated with decreased expression
                                                                                                                                                                                                                                                                                                                                                    Nguyen
Walia 1
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                                                                                                                                                             New human G-protein coupled receptors, useful for treatment and diagnosis of e.g. cell proliferation, also screening for specific modulators, and related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; neurological disorder; Huntington's disease; Parkinson's disease;
cardiovascular disorder; atherosclerosis; congestive heart failure;
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                                                                                                                                                                                                                                                                         WPI; 2001-616472/71.
N-PSDB; AAD19577.
                                                                                                                                                                                                                                                                                                                                                                                                   Policky JL,
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                                                                                                                                                                                                                                                                                                                                 NK, Das
                                                                                                           Page 101-102; 111pp; English.
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     sequence is a human G-protein coupled receptor, GCREC-1 e GCRECs are used for treating or preventing disorders with decreased expression of functional GCREC, and for
                                                                                                                                                                                                                                                                                                                                                                       Tribouley CM, Ta
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Au-Young J, Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local (
                                                                                                                                                           Human; CysLT2 GPCR; G-protein coupled receptor; oedema; asthma; immunological disorder; vascular disorder; reproductive disease; cellular metabolism; growth; development; blood; bone homeostasis; inflammation; allergy; angiogenesis; respiratory distress syndrome;
                                                         Key
                                                                                                                                                                                                                                                                                       07-MAY-2002
                                    Domain
                                                                                        Homo sapiens
                                                                                                                                     inflammation; allergy; angiogenesis; respiratory distress syndrome; Crohn's disease; blood pressure; protein therapy; anti-inflammatory;
                                                                                                                                                                                                                                                  Human CysLT2 GPCR (G-protein coupled receptor).
                                                                                                                                                                                                                                                                                                                          AAE17231;
                                                                                                                                                                                                                                                                                                                                                           AAE17231 standard;
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Pred. No. 2.7e-180;
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Query Match
Best Local Simi
Matches 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human CysLT2 GPCR (G-protein coupled receptor) polypeptide and its corresponding nucleic acid. The human CysLT2 GPCR, antibodies and compositions are useful for treating the human or animal body, or for diagnosing a disease. Human CysLT2 GPCR is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New HUMAN CysLT2 GPCR (G-protein coupled receptor), useful for diagnosing, preventing and treating inflammatory, immunological vascular disorders, e.g. asthma, allergy, angiogenesis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 346 AA;
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seventh transmembrane domains"
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The sequence represents a novel G-protein coupled receptor (GPCR), PFI-CC 017* of the invention. The PFI-017 has cytostatic, antiallergic, osteopathic, cardiovascular, and immunosuppressive activity. The cost-operatic cardiovascular, and immunosuppressive activity. The polymucleotides may have a use in gene therapy. The polymucleotide is useful for treating allergic disorders, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, an infectious disease, a neoplastic or myeloproliferative disease, or a heart disease. The cc allergic disorder is an allergic rhinitis or asthma, the pulmonary disorder is inflammatory disorder is inflammatory bowel disease. PFI-017 polymucleotide sequences may be used for the diagnosis of disease. PFI-017 polymucleotide sequences may be used for the diagnosis cc quantify gene expression in conditions, disorders or diseases in which PRI-017 activity may be implicated. The polypeptides are used to produce anti-PFI-017 antibodies to be used diagnostically to detect and quantify PRI-017 antibodies to be used diagnostically to detect and quantify compositions which can modulate the peptide can be used in treating obesity, diabetes and metabolic disease, neurological disease, urogenital cdisease, inflammation, cancer, osteoporosis, cardiovascular disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 7B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PFI-017 protein and polynucleotide encoding the protein, useful diagnosing or treating metabolic diseases, urogenital disease, immunological disorders, infectious diseases, , neoplastic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myeloproliferative diseases.
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19-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; GPCR; G prodrug development;
                                         Database global search for G protein-coupled receptors, encoded genes for studying in vivo signal transduction identifying targets for drug development.
                                                                                                                                                                                                                                                                                                                                           04-AUG-2000;
13-FEB-2001;
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2001JP-00034434.
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Pred. No. 2.7e-180;
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Claim 10; SEQ ID

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Matches 346
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                                                                                                                                                       Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder; fungal infection.
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Matches 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 582-583; 672pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders, cancer and promoting wound healing.
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                      NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                                                                                                                                          NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                      SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                               SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                                    NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPBSGLRV
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                                                                                                                                                                                                                                                           NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ 180
                                                                                                                                                                                                                                                                                                            YVFLQPYKKSTSVNVFMLNLAISDLLFISTLFFRADYYLRGSNWIFGDLACRIMSYSLYV
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V, Ujwal ML,
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Pred. No. 2.7e-180;
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Matches 346
                                                                                                                                             anti-ulcer, antiasthmatic, antiallergic, antinigraine, antiemetic, muscular, nootropic, anticonvulsant, immunostimulant, neuroprotective, neuroleptic, osteopathic and anti-HIV activities, and can be used in gene therapy and vaccine production. (I) and (II) can be used in diagnostic assays. They can also be used in identifying compounds that may be agonists or antagonists that are potentially useful in therapy, e.g. for treating bacterial, fungal, protozoan or viral infections (e.g. HIV-1), pain, cancers, diabetes, obesity; anorexia, acute heart failure, pain, cancers, diabetes, obesity; anorexia, acute heart failure, infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, dementia, or severe mental retardation or dyskinesias (e.g. Huntington's disease or Gilles de la Tourette's syndrome). (I) and (II) can also be used in vaccines for inducing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; LTD4-like G protein-coupled receptor; LTD4-like GPCR; antifungal; antibacterial; antiviral; protozoacide; analgesic; cytostatic; cardiant; hypotensive; hypertensive; antianginal; anorectic; anti-licer; nootropic; antiasthmatic; antiallergic; antimigraine; antiemetic; anticonvulsant; immunostimulant; neuroprotective; neuroleptic; osteopathic; anti-HIV; gene therapy; vaccine; infection; pain; cancer; diabetes; obesity; anorexia; acute heart failure; hypotension; hypertension; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy; benign prostatic hypertrophy; migraine; vomiting; dementia; dyskinesia; severe mental retardation; Huntington's disease; immunological response; gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the human LTD4-like G protein-coupled receptor (GPCR) protein (I). (I) and the polymucleotide (II) encoding it have antifungal, antibacterial, antivital, protozoacide, analgesic, cytostatic, cardiant, hypotensive, hypertensive, antianginal, anorectic,
                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 40; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New LTD4 receptor like G-protein coupled receptor polypeptide and polynucleotide, useful in diagnostic assays and in identifying agor or antagonists for treating infections, pain, cancer, hypertension.
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N-PSDB; ABA92899.
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  100.0%; ilarity 100.0%; Conservative 0
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  Score 1788; DB 5;
Pred. No. 2.7e-180;
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156. .1
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115. .
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SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF

300 240 240 180 180 120 120 60 60 0

NGSVTSCLELNLYKIAKLQTWAYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV

NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV

NMYSSIYFLTVLSVVRFLANVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ

YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV

YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV

MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI

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MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI

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This sequence represents a human CysL2-like G-protein coupled receptor CC (GPCR) protein of the invention. The invention comprises the DNA and Cprotein sequences of an isolated human CysLT2 (cysteinylleukotriene2)-CC like G protein-coupled receptor (GPCR) protein. This protein may have antibacterial, fungicide, virucide, cytostatic, anti-HIV, antianginal, CC explores of the protective, osteopathic, tranquiliser, nootropic, anti-CC inflammatory neuroprotective, antiparkinsonia, analgesic, cardiant, CC crebroprotective, antiasthmatic, antiallergic, antiarthritic and CC antiulcer activities. The invention also comprises an agent which CC inhibits the function of the CysLT2-like protein and is useful for treating CysLT2-like GPCR disorders. The protein and is useful for CC useful in raising specific antibodies which can block ligand binding, and CC are useful for treating disorders such as bacterial, fungal and viral CC virus, cancers, anorexia, bulimia, cardiovascular diseases (e.g. acute heart failure, angina, mycardial infarction), ulcers, osteoporosis, CC asthma, allergies, central and peripheral nervous system disease, a CC disease of the motor unit like neurogenic and myopathic disorders, CC motor neuron disease, dementia) also inflammatory diseases of the nervous system (e.g. arthritis and multiple sclerosis). The coding sequence of CC cysLT2-like GPCR golymucleotide is useful for generating antisense CC expression
  Query Match
Best Local Sim:
Matches 346;
                                                                             Sequence 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide, useful for treating peripheral or central nervous system, cardiovascular diseases and asthma, comprises the human cysteinylleukotriene2-like G protein-coupled receptor polypeptide.
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13-DEC-2000; 2000US-0254876P
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                    100
0%; Score 1788; DB 5;
0%; Pred. No. 2.7e-180;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obesity; human immunodeficiency virus infection; HIV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human G-protein coupled receptor HGPRBMY11 polypeptide or polynucleotide, useful for preventing, treating or ameliorating myocardial infarction, angina, thrombosis, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000; 2000US-0249613P
21-DEC-2000; 2000US-0257611P
16-JUL-2001; 2001US-0305818P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 33; Fig 6; 444pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schizophrenia, AIDS, leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-2001; 2001WO-US044019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G-protein coupled receptor HGPRBMY11v1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQUIBB
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HGPRBMY11 polypeptide
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  or polynucleotide
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Best Local S
Matches 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is also useful for treating, preventing or ameliorating e.g. Alzheimer's disease, Parkinson's disease, osteoporosis, obesity, human immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness, acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis, inflammations, psoriasis, Gaucher s disease or ischaemia (many other diseases and disorders are listed in the specification). The present sequence represents an HGPREMY11 protein (or variant)
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                                                                                                                                                                                                                                                                                                           YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346
NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV
                                                                                                     SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                      NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                                                                                                                                                               NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
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                                                                                                                                                                                                                                                                                                                                                            MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1788; DB 6;
Pred. No. 2.7e-180;
; Mismatches 0;
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RESULT 14
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hypertension; ulcer.

hypotension; renal disorder;

rheumatoid arthritis; trauma;

WO200261087-A2 Homo sapiens.

(LIFE-) LIFESPAN BIOSCIENCES INC 19-DEC-2000; 2000US-0257144P

2001WO-US050107

nervous system disease; asthma; cardiovascular disease; infection; HIV; cancer; bullmia; hypertension; osteoporosis; urinary retention; angina pectoris; allergy; ulcer; Parkinson's disease; pain; inflammation; neuroprotective; uropathic; gene therapy; human.

Human cysteinyl leukotriene

(CysLT2) - like GPCR protein

11-MAR-2004 ADH00945;

(first entry)

Homo

sapiens

Key

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The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino cc acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or a vidity for a particular GPCR. (I) can be used as GPCR modulators and in G gene therapy. The antigenic peptides for GPCRs are useful in detecting an CC antibodies. The peptides and antibodies are also useful for detecting the GPCRs and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antignic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell CC regeneration-related diseases, growth-related cell proliferative diseases, or autoimmune diseases, growth-related cell proliferative catherosclerosis, bacterial, fungal, protozoan or viral infections, costeoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host CC disease, Parkinson's disease, miltiple sclerosis, pain, psoriasis, cancer, epilepsy, asthma, tuberculosis, obesity, nausea, hyportension, concer, rheumatoid arthritis, trauma, ulcers, or cany other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ4523 to ABZ4869 encode CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 346;
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                                                                                                               SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF 300
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ilarity 100.0%;
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Pred. No. 2.7e-180;
); Mismatches 0;
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RESULT 15 ADH00945 ID ADH00 XX

ADH00945

standard;

protein; 346

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07-APR-2000;
11-DEC-2000;
09-APR-2001;
The invention relates to a cDNA encoding a human cysteinyl leukotriene (CysLT) -like G-protein coupled receptor polypeptide. The composition and methods are useful in disgnosing, preventing, ameliorating or treating dysfunctions or diseases, including peripheral and central nervous system disease, asthma or cardiovascular disease. These may also be utilised in infections (e.g. viral, bacterial, fungal or protozoan), HIV, cancer, bulimia, hypertension, osteoporosis, urinary retention, angina pectoris, allergies, ulcers, Parkinson's disease, pain, inflammation, etc. The CysLTZ-like GPCR may also be used in identifying test compounds for human GPCR modulators, such as agonists and antagonists, partial agonist, inverse agonist or co-activators. The protein and fragments may be used
                                                                                                                                                                                                                                                                                          New cDNA encoding a human cysteinyl leukotriene-like G-protein Coreceptor, useful for diagnosing, preventing or treating diseases peripheral or central nervous system disease, asthma, HIV or
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-787335/74.
N-PSDB; ADH00944, ADH00946.
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                                                                                                                                                                                                                                      Claim 4; SEQ
                                                                                                                                                                                                                                                                              cardiovascular disease.
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2000US-0254867P.
2001US-00828479.
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291. .:
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P47900 homo sapien Q6nsp5 homo sapien Aah69996 homo sapi

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MEDILINE=20459128; PubMed=10851239; DOI=10.1074/jbc.M003490200;
Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe
Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
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MEDLINE-20545741; PubMed-11093801;

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Kopatz S.A., Aronstam R.S., Sharma S.V.; cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
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Biochem. Biophys. Res. Commun. 274:316-322(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                   SEQUENCE FROM N.A.
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                   "Molecular cloning and characterization of a second human cysteinyl laukotriene receptor: discovery of a subtype selective agonist."; Mol. Pharmacol. 38:1501-1608 (2000).
                                                                                                                                                                       Civelli O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Submitted (SEP-2003)

to the EMBL/GenBank/DDBJ databases.

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RA Ainscough R. Jameida J. P., Ambrose K.D., Andrews D.T.,
RA Ainscough R. I. S., Babbage A.K., Bagguley C.L., Bailey J., Bannerjee R.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.B., Hammond S.,
RA Harley J.L., Hart B.A., Heath P.D., Howden P.J., Huckle B.J.,
RA Harley J.L., Hart B.A., Langford C.J., Johnson D., Kay M., Kimberley A.M.,
RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamorniert D.A.,
RA Moore M.J.F., Nickerson T., Palmer S.J., Nchurray A., Milne S.,
RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
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RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";

L'Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is LTC4 = LTP4 > LTP4.

C -!- SUBCELULAR LOCATION: Integral membrane protein.

C -!- TISSUB SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, spleen, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and classifications and submitted alightly in smooth muscle cells.
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GO; GO:0004974; F:leukotriene receptor activity; GO; GO:0006955; P:immune response; NAS. InterPro; IPR004071; Cysleuk receptor. InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
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AL137118; //
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AF254664;
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RESULT 2
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Best Local
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AAH69160;
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10-MAY-2004 (TIEMBLICEL 2
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CARBOHYD
CARBOHYD
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE; PS00237; G PROTEIN RECEP F1 1; F)
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1
G-protein coupled receptor; Glycoprotein;
                TISSUE=Synthetic constructs;
MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Primates;
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1. 27, Last annotation updat receptor 2.
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                                                                                                                          Catarrhini; Hominidae; Homo
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Pred. No. 1
                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
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STANDARD; PRT; 345 AA.

AC 095N03;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cysteinyl leukotriene receptor 2 (CysLTR2).

GN Name=CYSLTR2; Synonyms=CYSLT2;

Su scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Verteb

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Su

NCBL_TaxID=9823;

RN [1] _TaxID=9823;

RA Kamohara M., Takasaki J., Matsumoto M., Matsum
                                                                                                                                                                                                                                                                           RESULT
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Best Local S
Matches 346
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Submitted (APR-2004) to the
EMBL; BC069160; AAH69160.1;
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"Generation and initial analysis
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:
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                                                                         Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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Pred. No. 1e-
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(CysLTR2).
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Best Local (
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I pranty pro0401; 7tm 1; 1.

I PRO153; CYSLTRECPTR.

I PRO153; CYSCTRHODOPSN.

I PRO151; PS00237; G PROTEIN RECEP P1 2; 1.

I PRO151TE; PS00237; G PROTEIN RECEP P1 2; 1.

I PRO151TE; PS00237; G PROTEIN RECEP P1 2; 1.

I COMAIN

I G PRO151N RECEP P1 2; 1.

I CYCOPLASMIEM

I G CYCOPLASMIE (POTENTIAL).

I TRANSMEM 155 145 3 (Potential).

I TRANSMEM 155 175 4 (Potential).

I TRANSMEM 155 175 4 (Potential).

I DOMAIN

I 176 205 Extracellular (POTENAUSMEM 247 267 6 (Potential).

I TRANSMEM 247 267 6 (Potential).

I TRANSMEM 248 308 7 (Potential).

I TRANSMEM 288 308 7 (Potential).

I TRANSMEM 288 308 7 (Potential).

I DOMAIN

I 10 309 345 Cytoplasmic (Potential).

I DOMAIN

I 20 N-linked (GlCNAC)

CARBOHYD 20 N-linked (GlCNAC)

CARBOHYD 20 N-linked (GlCNAC)

CARBOHYD 20 N-linked (GlCNAC)

CARBOHYD 20 N-linked (GlCNAC)
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CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors.";
Submitted (DEC-2000) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB052662; BAB60817.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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79.3%;
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25; Mismatches
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N-linked (GlcNA
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N-linked (GlcNAc. ..) (Pol

N-linked (GlcNAc. ..) (Pol

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Extracellular (Potential).
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SEQUENCE
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Ogasawara H., Ishii S., Yokomizo T., Kakinuma T.,
Tamaki K., Shimizu T., Izumi T.,
"Characterization of Mouse Cysteinyl Leukotriene
mCysLT2. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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MGD; MGI:1917336; Cysltr2.
GO; GO:0016020; C:membrane; IDA.
GO; GO:0001631; F:cysteinyl leukotriene receptor activity; IDA.
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISTRIBUTION.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                       RAIFSKVH
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ilarity 73.4%;
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                            STANDARD;
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Pred. No. 2e-67;
0; Mismatches 52;
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AND TISSUE
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TRANSMEM
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-I- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylnositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: Widely expressed at low levels, with highest expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes.
-I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm_1; 1.

PRINTS; PR01533; CYSLTRECPTR.

PRINTS; PR00237; GPCORTHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1;

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2;

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1917336; Cysltr2.
GO; GO:0016020; C:membrane; IDA.
GO; GO:0001631; C:ysteinyl leukotriene receptor activity; IDA.
InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
Cysteinyl leukotriene receptor 2 (CysLTR2).
                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic cloning, alternative splicing, characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21601669; PubMed=11591709; DOI=10.1074/jbc.M107556200; Hui Y., Yang G., Galczenski H., Pigueroa D.J., Austin C.P., Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.; "The murine cysteinyl leukotriene 2 (CysLT2) receptor. cDNA an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse).
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                         Local Similarity
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                         66.9%;
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Score 1197; DI
Pred. No. 5.4e:
31; Mismatches
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Cytoplasmic
2 (Potential
                                                                                                                          By similarity.
N-linked (GlcNAc.
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7 (Potential).
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6 (Potential)
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Interpro; IPRUVUL.

Interpro; IPRUVUL.

Pfam; PF00001; 7tm 1; 1.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR01533; CVSLTRECPTR.

R PRINTS; PR01533; CFCRHODDOSN.

R PROSTTE; P800237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; P850262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 26 Extracellular (Potential).

FT TRANSMEM 27 47 1 (Potential).

FT TRANSMEM 27 47 1 (Potential).

FT TRANSMEM 27 47 2 (Potential).

FT TRANSMEM 37 2 (Potential).

FT TRANSMEM 48 56 Cytoplasmic (Potential).
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092479;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
CYSteinyl leukotriene receptor 2 (CYSLTR2) (RSBPT32).

Name=CYSLT2; Synonyms=CYSLT2;
Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptors.",
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Kamohara M., Takasaki J., Matsumoto M., Matsumoto S.,

Ohishi T., Soga T., Matsushime H., Furuichi K.;

"Characterization of the cloned rat and porcine cystei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGD; 619797;
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR004071; Cysleuk_receptor.
InterPro, IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB052661; BAB60816.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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SEQUENCE
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28-FEB-2003 (Rel. 41, Last sequence
01-OCT-2004 (Rel. 45, Last annotatio
Cysteinyl leukotriene receptor 1 (Cy
Name=Cysttrl, Synonyms-Cystt;
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                                                                                                  SEQUENCE FROM N.A.
Takasaki J., Kamor
Ohishi T., Soga T.
                                                                                                                                                 Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Rod
                                                                                                                                      NCBI_TaxID=10116;
                                                                                          Characterization
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                                                                                       T., Soga T., Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                         ra M., Saito T., Matsumoto M., Mat
Matsushime H., Furuichi K.;
f cloned rat and porcine cysteinyl
                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1119
1137
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167
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73.1%;
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Cytoplasmic (Potential).

4 (Potential).

Extracellular (Potential).

5 (Potential).

Cytoplasmic (Potential).

6 (Potential).

Extracellular (Potential).

7 (Potential).

Cytoplasmic (Potential).

7 (Potential).

Y (Potential).

17 (Potential).

N-linked (GlCNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1187; DB 1;
Pred. No. 2.3e-66;
6; Mismatches 57;
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linked (GlcNAC...) (P-linked (GlcNAC...) (P-linked (GlcNAC...) (P-linked (GlcNAC...) (P-A122AC8177879D56 CRC64;
                                                                                                                                                                                       ation update)
(CysLTR1).
                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODODSN.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50362; G PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Glycoprotein; Transmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                     315
                                                                                                                                            247
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                    RLKSALRK-----GHPQKAKTKC 332
                                                                                                                                          SFMPYHIQRAIHLHFLHSETRSCDSVLRMQKSVVITLSLAASNCCFDFLLYFFSGGNFRR
                                                                                                                                                          CFLPYHTLRTVHL--TTWKVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKD
                                                                                                                                                                                                                                     FPVQNINLVTQKKARFVCVGIWIFVILTSSPFLLSKSYQDEKNNTKCFEPPQDKQTKKYV
                                                                                              RL-STFRKHSLSSMTYIPKKKASLPEKGEEMC
                                                                                                                                                                                         LVLHYVSLIFGFIIPFVTIIVCYTMIILTLLKNTMKKN--LPSRRKAIGMIIVVTAAFLV
                                                                                                                                                                                                    HPFRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--L
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109
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144
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1196
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98
 (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                    STANDARD;
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Extracellular (Potential).
7 (Potennial).
Cytoplasm:
                                                                                                                                                                                                                                                                                                                                                                              70; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential)
5 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).

By similarity.

N-linked (GlcNAc...) (Potential).

N-linked (GlcNAc...) (Potential).

N-linked (GlcNAc...) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                         Score 567.5; DB 1;
Pred. No. 8.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular (Potential)
3 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic 2 (Potential
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                                    PRT;
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                                   340
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 339;
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                                                                                                                                                                                         246
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Matches 116
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                      G-protein
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01533; CTSLTRECPTR.
PRINTS; PR00237; GPCKRHODODSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS00252; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takasaki J., Kamohara M., Saito T., Matsumoto M
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of cloned rat and porcine cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (Rel. 44, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLTR1).
Name=CYSLTR1; Synonyms=CYSLT1;
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB052686; BAB60826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Receptor for cysteinyl leukotrienes mediating constriction of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00001;
  72
                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an
                                                                                                                Similarity
                                                 DILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHP
DILCYCTLPLRYVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFWTAMSFFRCIAIVFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           email to license@isb-sib.ch).
                                                                                                                                                    340
                                                                                                    Conservative
                                                                                                                                                                              166
197
218
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234
255
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280
301
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172
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A
                                                                                                                                                     265
38986
                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                              31.5%;
                                                                                                                                                    MW;
                                                                                                                                                         Cytoplasmic (Potential).
By similarity.
N-linked (GlcNAc. . .) (
                                                                                                   75;
                                                                                                 Score 563; DB
Pred. No. 1.6e-
75; Mismatches
                                                                                                                                                                                                                                          Extracellular (Potential).
7 (Potential).
                                                                                                                                                                                                                                                                Cytoplasmic 6 (Potential
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4 (Potential)
                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic 2 (Potentia:
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                                                                                                                                                                                                                                                                                                                                          (Potential)
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                                                                                                              DB 1;
.6e-27;
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                                                                                                                         Length 340;
                                                                                                                                                    CRC64;
                                                                                                    Indels
                                                                                                                                                                (Potential).
) (Potential).
) (Potential).
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RESULT
CHAPTER
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C 099JA4; 099J71; 099JK47;

T 28-FEB-2003 (Rel. 41, Created)

T 28-FEB-2003 (Rel. 41, Last sequence update)

T 05-JUL-2004 (Rel. 44, Last annotation update)

C Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl 1 E receptor) (LTD4 receptor).

E Name=Cysltr1; Synonyms=Cyslt1, Cysltlr;

Mus musculus (Mouse).

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN-Czech II, TISSUE-Mammary gland;

MEDLINE-2388257, pubmed-12477932; DOI-10.1073/pnas.242603899;

MEDLINE-2388257, pubmed-12477932; DOI-10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (12)
SEQUENCE FROM N.A. (ISOFORM 1/.
STRAIN=C57BL/6; TISSUE=Trachea;
MEDLINE=21562332; PubMed=11705452; DOI=10.1016/S0006-2952(01)00774-2;
MEDLINE=21562332; PubMed=11705452; DOI=10.1016/S0006-2952(01)00774-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mollerup J. Jorgensen S.T., Hougaard C., Hoffmann B.K.; "Identification of a murine cysteinyl leukotriene receptor by expression in Xenopus laevis occytes."; Biochim. Biophys. Acta 1517:455-459(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and functional characterization cysteinyl-leukotriene 1 (CysLT1) receptors."; Biochem. Pharmacol. 62:1193-1200(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maekawa A., Kanaoka Y., Lam B.K., Austen K.F., "Identification in mice of two isoforms of the creceptor that result from alternative splicing." Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                  Ogasawara H.,
Submitted (MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21240338; PubMed=11342226; DOI=10.1016/S0167-4781(00)00271-2; Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann E.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11226226; DOI=10.1073/pnas.041624398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Izumi
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the EMBL/GenBank/DDBJ
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; "eneration and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences."; "roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: Receptor for cysteinyl leukotrienes mediating constriction of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4 constitution of the Constitution of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein constitution of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein constitution of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein constitution of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein constitution of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein constitution of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein constitution of the microvascular smooth muscle during an inflammatory response in microvascula
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: Widely expressed, with higher expression in the lung and skin, intermediate levels in the heart, kidney and stomach and lower levels in several other tissues. Isoform 1 is the most abundant form in all tested tissues.

MISCELLANEOUS: MK-571, a selective antagonist, was shown to inhibit eosinophilia, bronchial hyperreactivity and microvascula leakage. Zafirlukast (Accolate) and pranlukast (Onon) were also shown to be selective antagonists.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1; Synonyms=Long; IsoId=Q99JA4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ame=2; Synonyms=Short;
IsoId=Q99JA4-2; Sequence=VSP_001921;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ere are no restrictions as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.isb-sib.ch/announce/
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GO; GO:0005887; C:integral to plasma membr
GO; GO:0004974; F:leukotriene receptor act
GO; GO:0007166; p:cell surface receptor li
InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pf00001; 7tm l; l.—
PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; GPCRRHODDPSN.
PROSITE; PS00237; GPCRHODDPSN.
Alternative splicing; G-protein coupled re
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF329272; AAK16715.1; -.
EMBL; AF329272; AAK16716.1; -.
EMBL; AF329372; AAK16733.1; -.
EMBL; AF205830; AAK15433.1; -.
EMBL; AF263370; AAF73047.1; -.
EMBL; AF263370; BAAF36809.1; -.
EMBL; AE027102; AAH27102.1; -.
EMBL; BC027102; AAH27102.1; -.
HSSP; P34996; 1DDD.
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ene receptor activity; IDA.
face receptor linked signal transdu. .
Extracellular (Potential).

1 (Potential).

Cytoplasmic (Potential).

2 (Potential).

Extracellular (Potential).

3 (Potential).

Cytoplasmic (Potential).

4 (Potential).

Extracellular (Potential).

5 (Potential).
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Matches 117
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CARBOHYD
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last amnotation update)
Adult male colon cDNA, RIKEN full-length enriched library,
clone:9030217A18 product:CYSTEINYL LEUKOTRIENE 1 RECEPTOR
ISOFORM, full insert sequence.
            RIKEN
                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                              the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                            BAC28308;
                                                                                                                                                        NCBI_TaxID=10090;
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Rodentia;
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of a full-length mouse cDNA collection.";
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N-linked (GlCNAc...) (I

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Missing (In isoform 2).

/FTId=VSP 001921.

Y > D (in Ref. 3).
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Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
By similarity.
N-linked (GlcNac. . .) (Potential).
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9; Mismatches
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Pred. No. 2.6e-27;
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Sciurognathi; Muridae;
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2 STRAIN-C57BL/61; TISSUE-Colon;

2 STRAIN-C57BL/61; TISSUE-Colon;

3 Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

4 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

5 Fukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,

6 A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

7 A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

8 A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

8 A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

8 A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

8 A Kurihara C., Matsuyama T., Miyazaki A., Ohno M., Ohsato N., Okazaki Y.,

8 A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

8 A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

9 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

9 A Tagawa A., Takahashi F., Takaku Akahira S., Takeda Y., Tanaka T.,

10 A Tagawa A., Takahashi F., Takaku Akahira S., Takeda Y., Tanaka T.,

11 A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayasshizaki Y.;

12 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Alzawa K., Kitsunai T., Tashiro H., Itoh M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakupuni S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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STRAIN-C57BL/6J; TISSUB=Colon;
MEDLINE=20499374, PubMed=11042159;
Carninoi P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=99279253; PubMed=10349636;
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                                                                                                                                                                                                                          NNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDL
YHIQRTIHLHLLHSETRPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRRRL
                     YHTLRTVHLITTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLKS
                                                                          YVSLFFGFIIPFVTIIVCYTMIILTLLKNTMKKN
                                                                                                                                                 NINLYTOKKARFYCIGIWIFYILTSSPFLMYKSYQDEKNNTKCFEPPQNNQAKKYVLILH
                                                                                                                                                                                   LLHVTSIRSAWILCGIJWI-LIMASSIMLLDSGSBQNGSVTSCLELNLYKIAK--LQTWN
                                                                                          YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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.6e-27;
                                                                          --MPSRRKAIGMIIVVTAAFLVSFMP
                                                                                                                                                                                                                                                                                                                                                                              108;
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CLT1_HUMAN
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Q9Y271;
 the Europuse by modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sarau H.M., Ames R.S., Chambers J., Ellis C., Elshourbagy N., Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdock P.R., Herrity N.C., Halsey W., Sathe G., Muir A.I., Nuthulaganti P., Dytko G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P.; "Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor.";
                                                       This SWI
between
                                                                                                                                                                                                                                                                                                          "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (PEB-2003) to the EMBL/GenBeak/DBJ databases.

-I- FUNCTION: Receptor for cysteinyl leukotrienes mediating bronchoconstriction of individuals with and without asthma. Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, edema, eosinophil migration and damage to the mucus layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLTR1) (Creceptor) (LTD4 receptor) (HG55) (HMTMF81).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Leukocyte, Peripheral blood
MEDLINE=99393629; PubMed=10462554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99318129; PubMed=10391245;
Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Mett
Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connoll
Bai C., Austin C.P., Chateauneuf A., Stocco R., Greig G.M.,
Kargman S., Hoose S.B., Hosfield E., Williams D.L. Jr.,
Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;
"Characterization of the human cysteinyl leukotriene CysLT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Warren C.N., Arons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CYSLTR1; Synonyms=CYSLT1;
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                     European
by non-
                                                                                                      and heart.
MISCELLANEOUS: Selective antagonists, such as montelukast
(Singulair), zafirlukast (Accolate) and pranlukast (Onon), are
used in the treatment of the asthma crisis.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                      >> LTE4 = LTC4 >> LTB4.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed, with highest levels in spleen and peripheral blood leukocytes. Lower expression in several tissues, such as lung (mostly in smooth muscle bundles)
SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is fied and this statement is not removed. Usage by and for
                                                                                                                                                                                                    alveolar macrophages), placenta, small intestine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocytes,
                 There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                              iated via a G-protein
second messenger
leukotrienes is LTD4
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Matches
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GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0004974; F:leukotriene receptor activity; TAS.
GO; GO:0004974; F:cycosolic calcium ion concentration ele
GO; GO:0007204; P:cycosolic calcium ion concentration ele
GO; GO:0007585; P:respiratory gaseous exchange; TAS.
GO; GO:0007585; P:respiratory gaseous exchange; TAS.
InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR004071; Cysleuk_receptor.
RINETS; PR000017; TTM, 1 1.
PAINTS; PR000017; TTM, 1 1.
PRINTS; PR00133; CYSLITRECPTR.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; 
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EMBL; AF313266; AAD42778.1; -
EMBL; AY242130; AAO92297.1; -
HSSP; P34996; IDDD.
Genew; HGNC:17451; CYSLTR1.
MIN; 300201; -
GO; GO:0005887; C:integral to
GO; GO:0005887; C:membrane fr.
GO; GO:0005624; C:membrane fr.
GO; GO:0007504; P:cytosolic c.
GO; GO:0006952; P:cespiratory
GO; GO:00067585; P:cespiratory
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CARBOHYD
CARBOHYD
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or send an email to license@isb-sib.ch).
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                                                                                                                                                      NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                                                               RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM
                                                                                                                                                                                                                                                                                                                               LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF
STFRK
                                      SALRK 322
                                                                                                               PYHTLRTVHLTTW--KVGLCKD-
                                                                                                                                                                                                                                                                                                                                                                                        SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD
                                                                                                                                                                                                                                                                                                               LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV
                                                                             PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITI
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By similarity.
N-linked (GlONAc. . ) ()
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Pred. No. 2.9e-27;
1; Mismatches 106
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2 (Potential).
Extracellular (Potential).
3 (Potential).
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Matches 115
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XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Lington M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Lington M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Lington M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

XX Lington M., Guellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Rillalon D.K., Mozny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XX Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XX Pahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,

XX Alaksley R.W., Touchman J.W., Green E.D., Dickson M.C.,

XX Alaksley R.W., Touchman J.W., Green E.D., Dickson M.C.,

XX Alones S.J., Marra M.A.;

XX Alones S.J., Marra M.A.;
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01-JUN-2003
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC035750; AAH35750.1; -.

GO; GO:0016021; C:integral to membrane; IEA,
GO; GO:0004974; F:leukotriene receptor activity; IEA,
GO; GO:0004872; F:receptor activity; IEA,
GO; GO:0007186; P:G-protein coupled receptor
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Pancreas;
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115; Conserv
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                                              RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM
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; Primates;
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Pred. No. 6.8e-27;
1; Mismatches 107
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Catarrhini;
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SEQUENCE FROM N.A.

MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;

"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GP80_HUMAN STANDARD; PRT; 337 AA.

996F68; Q86TL1;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

Probul-2 (Rel. 44, Last annotation update)

Probuble G protein-coupled receptor GPR80 (P2Y-like receptor) (P2Y-like GPCR).

Name=GPR80; Symonyms=GPR99;
                                                                                                                                                                                                 Suwa M., Sato T., Okouchi I
Tsutsumi S., Aburatani H.,
"Genome-wide discovery and
                                                                                                                                                                                                             [4]
SEQUENCE FROM N.A.
Seto T., Okouchi I.,
ABI
                                                                                                                                                                                                                                                           genome sequence.";
FEBS Lett. 520:97-101(2002)
                                                                                                                                                                                                                                                                                                                                          "GPR99, a new G protein-coupled of nucleotide receptors."; BMC Genomics 3:17-17(2002).
                                                                                             Submitted
                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Thyroid;
                                                                                                                                                                                                                                                                              MEDLINE=22040266; PubMed=12044878;
Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku
"Identification of G protein-coupled receptor genes
                                                                                                                                                                                                                                                                                                                                                                             Wittenberger T., Hellebrand S., Munck A., Schaller H.C., Hampe W.;
                                                                                                      receptor.
                                                                                                                 Bruess M., Bonisch
"Molecular cloning
                                                                                                                              Bruess M.,
                                                                                                                                                                           Submitted
                                                                                                                                                                            receptor genes.";
Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12098360;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                            FUNCTION: Orphan receptor
SUBCELLULAR LOCATION: Integral m
TISSUE SPECIFICITY: Detected in
placenta. Not detected in brain
            pons.
SIMILARITY:
                                 cortex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    275:83-91 (2001).
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           G-protein
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/ama Y.;
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Query Match
Best Local S
Matches 111
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EMBL; AF370886; AAM76912.1; -
EMBL; AB083598; BAB83311.1; -
EMBL; AB065877; BAC06095.1; -
EMBL; AJ305372; CAC83857.1; -
Genew; HGNC:4531; GPR80.
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PRINTS; PR00237; GFCRHODDESN.

PROSITE; PS00237; G PROTEIN RECEP F1 2; 1:

PROSITE; PS002362; G PROTEIN RECEP F1 2; 1:

G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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InterPro; IPR002286; P2_pt
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                          NCTIEN--FKREFFPIVYLIIFFWGVLGNG--LSIYVF-LQPYKKSTSVNVFMLNLAISD
AVCSTVRCKVSGNLEQAK
                                              RLLHVTSIRSAWILCGIIWILIMASSI---MLLDSGSEQNGS----VTSCLELNLYKIAK
                                                                                                                                                                                            LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYYNWYSSIYFLTVLSVVRFLAWVHPF
                    RLKSALR---KGHPQKAK
                                                                   LCFLPYHTLRTVHLTTWKVGL---CKDRLHKALVITLALAAANACFNPLLYYFAGENFKD
                                                                                             --WYNLILTATTFCLPLVIVTLCYTTIIHTLTHGLQTDSCLK---
                                                                                                                   LQTMNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITTLIFF
                                                                                                                                           SCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIK---
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337
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2 (Potential).
Extracellular (Potential).
3 (Potential).
3 (Potential).
4 (Potential).
4 (Potential).
5 (Potential).
Extracellular (Potential).
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
7 (Potential).
Extracellular (Potential).
7 (Potential).
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By similarity.
N-linked (GlcNAc. .) (Pot
F -> L (in Ref. 5).
K -> R (in Ref. 5).
                     329
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Pred. No. 8.1e-23;
4; Mismatches 114;
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F1_2; 1.
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RESULT 14
GP17_HUMAN STANDARD;
ID GP17_HUMAN STANDARD;
AC 01304;09UDZ6; 09UBZ1;
DT 01.NOV-1997 (Rel. 35, Created DT 28-FEB-2003 (Rel. 44, Last an DE PCDAD 140;004 (Rel. 44, Last an DE PCDAD 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBOID-Q13304-2; Sequence=VSP_001987;
-!- TISSUE SPECIFICITY: Primarily expressed in brain.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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                                                                                                                                                                       PROSITE; PS00237; G PROTEIN RECEP F1 1; PROSITE; PS50262; G PROTEIN RECEP F1 2; Alternative splicing; G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blaesius R.H., Weber R.G., Lichter P., Ogilvie A., Manovel orphan G proteain-coupled receptor primarily rain is localized on human chromosomal band 2q21.", J. Neurochem. 70:1357-1365(1998).
                                                                                                                                                                                                                                                      GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002286; P2 purnocptor.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00227; GPCRRHODOPSN.
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MEDLINE-96145150; PubMed-8558062;
Raport C.J., Schweickart V.L., Chantry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
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t annotation update)
GPR17 (P2Y-like receptor)
     Extracellular (Potential).

1 (Potential).

Cytoplasmic (Potential).

2 (Potential).

Extracellular (Potential).
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Best Local S
Matches 116
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01-OCT-2002
01-MAR-2004
GPR17 protei
MEDLINE-22386257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.; Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S./
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Mammalia; Eutheria;
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                                                                                                                                                         SEQUENCE FROM N.A.
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116; Conserv
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Primates;
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Pred. No. 1.3e-22;
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/FTId=VSP_001987.
; 132FBE97BE83C60C CRC64;
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g (in isoform 2).
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Best Local
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PRINTS; PR00237; GFCRHODOPSN.

PRINTS; PR01157; PS2YPURNOCPTR.

PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.

PROSITE; PS00237; G PROTEIN_RECEP_F1 2; 1.

PROSITE; PS50262; G PROTEIN_RECEP_F1 2; 1.

PROSITE; PS50262; G PROTEIN_RECEP_F1 2; 1.
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G0; G0:0016021; C:integral to membrane; IEA.
G0; G0:0045028; F:purinergic nucleotide receptor act
G0; G0:0045028; F:rhodopsin-like receptor activity;
G0; G0:0007186; F:rhodopsin-like receptor protein
InterPro; IPR002276; GPCR Rhodops.
InterPro; IPR002286; P2_purnocptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
"Generation and initial analysis of
"Generation and initial analysis of
and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:168
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MYFFVAEKFRHALCNLLCGKRLKGPPPSFEGK
                            LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
                                                           MIAIVLAIFLVCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPI
                                                                                                                                          NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR----KALT
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                                                                                      TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACENPL
                                                                                                                     -LYR-EKASHHALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR
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Pred. No. 1.
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earch completed: December 13, 2004, 17:52:34 ob time : 191 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MERKFMSLQPSISV
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Gapop 10.0 , Gapext 0
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573.651 Million cell updates/sec
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            US-09-585-876-2
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US-09-586-924-2
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US-09-19-110-32
PCT-US95-07180-2
US-08-113-9748-374
US-08-113-9748-374
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US-08-113-9748-374
US-08-13-9748-474-4
US-08-152-524A-4
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US-08-152-524A-4
US-08-152-524A-4
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Sequence 2, Appli
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Sequence 17, Appli
Sequence 4, Appli
Sequence 7, Appli
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Sequence 18, Appli
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d dd	95 AG	B & B &	Query Mat Best Loca Matches Qy Db	28 29 30 30 31 4 31 31 31 32 4 33 34 34 34 34 41 41 42 43 44 44 45 44 45 47 45 47 47 47 48 48 48 49 49 49 40 41 41 41 41 41 41 41 41 41 41 41 41 41
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AGENFKDRLKSALRKGHPOKAKTKCVFPVSVWLRKETRV 	MYIALVVGCLLPFFTLSI 	SDLLFISTLPFR	99.5%; Score 1779; DB 4; Length 99.4%; Pred. No. 3.7e-131; tive 1; Mismatches 1; Indel ISVSEMEPHGTFSNNNSRNCTIENFKREFFPIVYL	3 US-08-467-947A-8 4 US-09-170-496D-206 4 US-09-745-642-17 4 US-09-745-842-15 3 US-08-513-974B-373 4 US-09-102-710B-3 3 US-08-988-876-9 1 US-08-442-134A-2 1 US-08-444-08BA-2 2 US-08-559-524A-3 3 US-08-947-922-3 4 US-08-947-922-3 4 US-08-097-938-6 1 US-08-476-000-6 1 US-08-476-000-6 2 US-08-476-976-6
₹V 346 346	CYLLITRYLLKVEVPESGLRV			Sequence 8, Appli Sequence 206, App Sequence 17, Appli Sequence 15, Appli Sequence 373, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli
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APPLICANT: SHALL,
TITLE OF INVENTION: A NOVEL HUMAN 7-INALL,
TITLE OF INVENTION: A NOVEL HUMAN 7-INALL,
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRE
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APPLICANT: SATHS,
APPLICANT: HALSEY,
APPLICANT: ELLIS, C
APPLICANT: AMES, RO
APPLICANT: FOLEY,
APPLICANT: SARAU, H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                          190
                                                                                                                                                                                                                               130 QNINLVTQKKARFVCVGiWiFVILTSSPFLMAKPQKDGKNNTKCFEPPQDNQTKNHVLVL
                                                                                                                                                                                                                                                                                              145 RLLHVTSIRSAWILCGIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116;
                                           262
                                                                                                                                                                202 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 261
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                                                                                                                                                                                                                                                                                                                                                                                                  85 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF
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PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACENPLLYYFAGENFKDRLK 317
                                                                                                HYVSLFVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM
                                                                                                                                                                                                                                                                                                                                                              LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFWTAMSFFRCIAIVFPV 129
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HALSEY, WENDY
ELLIS, CATHERINE
AMES, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.3%; Score 559; DB 3; Length 337; ilarity 38.0%; Pred. No. 3.6e-36; Conservative 71; Mismatches 106; Indels
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SARAU, HENRY
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A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09/044,404A
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                              APPLICANT:
APPLICANT:
          APPLICANT:
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SOFTWARE: PASTSEQ FOR WI
SEQ ID NO 2
LENGTH: 337
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-586-924-2
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TITLE OF INVENTION: CDMA CLONE HMTMF81 THAT ENCODES A NOVEL
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
FILE REFERENCE: GH-70001-1D1
CURRENT APPLICATION NUMBER: US/09/586,924
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1997-04-22
NUMBER: PASTARE: FASTSEQ for Windows Version 3.0
                                                                                                                           RESULT 4
US-08-153-848-44
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US-09-586-924-2
                                                            Sequence 44, Application US/08153848 Patent No. 5759804 GENERAL INFORMATION:
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Best Local Similarity 38.0%;
Matches 116; Conservative 71
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APPLICANT: SATHE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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5. 6506878
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                                                                                                                                                                                                                                                                                                                              PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAAAACENPLLYYFAGENFKDRLK 317
                                                                                                                                                                                                                  STFRK 311
                                                                                                                                                                                                                                                             SALRK 322
                                                                                                                                                                                                                                                                                                                                                                                          HYVSLFVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM
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HALSEY, WENDY
ELLIS, CATHERINE E
AMES, ROBERT S.
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Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Mismatches 106;
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US-08-812-871-3
                                                                                                          RESULT 5
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Sequence 3, Application US/08812871
Patent No. 5955303
GEMERAL INFORMATION:
APPLICANT: Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,45
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (312) 474-04
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 339 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y Match 27.0%;
Local Similarity 34.6%;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                 248
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amino acid
OGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLEL 190
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                                                                                                                                                                                                                                                                                                                                       -LYR-EKASHHALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
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Bicknell
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  RESULT 6
US-09-299-843A-44
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Best Local Similarity 34.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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APPLICANT: Muzong Ch
TITLE OF INVENTION: I
TITLE OF INVENTION:
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LIBRARY: GenBa
CLONE: 992700
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NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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CITY: Palo Alto
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                                 304 LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
                                                                                                     248 TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPL 303
                                                                                                                                           184 - LYR-EKASHHALVSLAVAFTFFFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR
                                                                                                                                                                   191 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPBSGLRVSHR----KALT
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                                                                     236 MIAIVLAIFLVCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDFI
                                                                                                                                                                                                                                                                                      65 PANVFLMHLAVADLSCVLVLFTRLVYHESGNHWEFGEIACRLTGFLFYLNMYASIYFLTC
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MYFFVAEKFRHALCNLLCGKRLKGPPPSFEGK 327
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Muzong Cheng
NVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
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Pred. No. 2.7e-30;
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Best Local Similarity
Matches 115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: 9111 E. Uhl
REGISTRATTON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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APPLICATION NUMBER:
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                                                                                                                                                         125 ISADRPLAIVHPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ-
                                                                                                                                                                                          132 LSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLEL 190
                                        248 TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPL 303
                                                                                                                                                                                                                                        65 PANVFLMHLAVADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTC 124
                                                                                                                                                                                                                                                                          72 SVNYFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTV 131
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NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALT
                                                                              -LYR-EKASHHALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
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6300 Sears Tower,
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44
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US-09-088-337B-44
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                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Godiska, Ronald
191 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR----KALT 247
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                                                                                                                                      65 PANVFLMHLAVADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTC
                                                                                                                                                             72 SVNVFMLNIAISDLLFISTLFFRADYYLRGSNWIFGDIACRIMSYSLYVNMYSSIYFLTV 131
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                                                                                LSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLEL 190
                                                            ISADRFLAIVHPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ- 183
                                                                                                                                                                                                                     EVAPPGLITNESLATAEQCGQETPLENMLEASEYLLDEILALVGNTLALWLEIRDHKSGT
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                 27.0%;
ilarity 34.6%;
Conservative 63
                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                                                                                                                                 Score 483.5; DB 3;
Pred. No. 2.7e-30;
3; Mismatches 129;
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RESULT 9
PCT-US93-11153-44
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, App
Patent No. 65553
                                                                                                                                                                  Sequence 44, Application PC/TUS9311153 GENERAL INFORMATION:
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Best Local (
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09-170-496D-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen M.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
                                   APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                       304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 - LYR-EKASHHALVSLAVAFTFFFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
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                                                                                                                                                                                                                                                                                                                                       LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLEL 190
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  Marshall, O'Toole, Gerstein, Murray & Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.0%; Score 483.5; DB 4; 34.6%; Pred. No. 2.7e-30; tive 63; Mismatches 129;
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                                                                                                                                                                                      RESULT 10
PCT-US95-07180-2
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                                                                                                                    Sequence 2, Application PC/TUS9507180
GENERAL INFORMATION:
APPLICANT: LI, YI
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Best Local Similarity
Matches 115; Conserv
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                                       APPLICANT: LI, YI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
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CITY: C
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TELEX: 25-3856
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                   304 LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVAPPGLITNESLATAEOCGOETPLENMLEASEYLLDEILALVGNTLALWLEIRDHKSGT
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  CARELLA,
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BYRNE,
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  BAIN,
                                                               RECEPTOR
  GILFILLAN, CECCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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295

ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND

COUNTRY: UZIP: 07068

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RESULT 11
US-09-170-496D-182
; Sequence 182, Application US/09170496D
; Patent No. 6555339
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Best Local S
             APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous,
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vere
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
NUMBER OF
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REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 32!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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FILING DATE: 06-JUNE-199
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 339 amino acids
TYPE: amino acid
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SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                         MYFFVAEKFRHALCNLLCGKRLKGPPPSFEGK 327
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PILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JE
PILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:

PCT/JP95/01599

PRIOR APPLICATION DATA

APPLICATION NUMBER: FILING DATE: 19-AUG

19-AUG-1995

JP 7-093989

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US-08-513-974B-374
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SEQ ID NO 182
LENGTH: 339
TYPE: PRT
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Best Local Similarity
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APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Plopy disk
COMPUTER: PROCOMPATION
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/513,974B
                                                                                                                                                                                                                                                                                                  APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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CITY: E
                                                                                                                                        COUNTRY: US
ZIP: 02109
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Hosoya, Masaki
Fujii, Ryo
Ohtaki, Tetsuya
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                                                                                                                                                               USA
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Pred. No. 4.6e-30;
2; Mismatches 130
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RESULT 13
US-08-781-250-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 45
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FILING DATE: 11-AUG-1945
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                                                                                    CFNPLLYYFAGENFKDRLKSALRK 322
                                                                                                                                   ALTTIIITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANA 298
                                                                                                                                                                           TADEYLRSYFVYSMCTTVFMFCI----PPIVILGCYGLIVKALIYKDLDNSPLR---RK
                                                                                                                                                                                                                                    VHRYTGVVHPLKSLGRLKKKNAVYVSSLVMALVVAVIAPILFYSGIGVRRNKTIT-CYDT 194
                                                                                                                                                                                                                                                                  VVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE- 189
                                                                                                                                                                                                                                                                                                                                                       ELLAGGWAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRFWSGI
                                                                                                                                                                                                                                                                                                                                                                                  EMEPNGTFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSV 73
                                                       CVDPILYFLAGDTFRRRLSRATRK 330
                                                                                                                  STYLVIIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNS 306
                                                                                                                                                                                                     -----LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRK 244
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30-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                 82; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 464; DB 3;
Pred. No. 9.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 362;
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US-08-781-250-2
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FILING DATE: 10-JAN-1997
CLASSIFICATION DATA:
APPLICATION MATA:
APPLICATION NUMBER: 1514
PRIOR APPLICATION MATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.0%; Score 447.5; DB 3; Best Local Similarity 31.6%; Pred. No. 1.9e-27; Matches 109; Conservative 74; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08781250 Patent No. 6010877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Sathe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 370 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: William T. Han,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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299
                                      293 LAAANACFNPLLYYFAGENFKD-----RLKSALRKGHPQKAK 329
                                                                                                                                                     180 NVNNATTTCFEGFSKRVWKTYLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLS
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LATLNCCFDPFIYYFTLESFQKSFYINAHIRMESLFKTETPLTTK 343
                                                                                                            GLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCK---DRLHKALV-ITLA
                                                                                                                                                                                                                                   LFVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKI-FYNFNRHWPFGDTLCKISGTAFL
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                                                                           QIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAITNCFLERFAKIMYPITLC
                                                                                                                                                                                            EQNGSVTSCLELNLYKIAK--LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVBVPES
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709 Swedeland Road
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Van Horn, Stephanie
Bergsma, Derk
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RESULT 15
US-08-559-524A-4
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US-09-745-842-14
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US-09-745-842-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SOFTWARE: PatentIn Ver.
SEQ ID NO 14
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
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APPLICANT: COR Therapeutice, Inc.
TITLE OF INVENTION: P2Y12 Receptor
FILE REFERENCE: 44481-5053-US
CURRENT APPLICATION NUMBER: US/09/745,842
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 60/171,622
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                        Sequence 4, Application US/08559524A Patent No. 5871963
GENERAL INFORMATION:
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Matches 102; Conservative
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Best Local Similarity
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                                                                                      APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STATE: D.C. COUNTRY: US. ZIP: 20036-
                                                  STREET: 1800 M St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                              324 YFLAGDTFRRRLSRATRK 341
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20036-5869
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Jantzen, Hans-Michael
Ramakrishnan-DuBridge, Vanitha
                                                                          B: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
                    USA
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Pred. No. 2.5e-27;
9; Mismatches 111; Indels
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Search completed: December 13, 2004, 17:54:06 Job time: 42 secs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNDRER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 044481-501
REFERENCE/DOCKET NUMBER: 044481-501
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Local Similarity 31.0%; Pred. No. 5.1e-27;
les 95; Conservative 78; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKTGFQFYYLPAVYILVFTIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTL 104
                                                                                      SRATRK
                                                                                                                             KSALRK 322
                                                                                                                                                                                                                  YHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL
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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 ,
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1788
1 MERKFMSLQPSISVSEMEPN.....KAKTKCVFPVSVWLRKETRV 346
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1: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOME.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOME.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-09-866-230-7
US-09-866-230-9
US-09-828-478-2
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US-09-979-679-26

US-09-991-225-30

US-09-980-049-1

US-10-225-567A-589

4 US-10-349-021-2

US-10-349-021-2

US-10-313-332A-2

US-10-131-332A-2
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Sequence 6, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 26, Appli
Sequence 36, Appli
Sequence 30, Appli
Sequence 1, Appli
Sequence 589, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 14, Appli
Sequence 2, Appli
Sequence 30, Appli
Sequence 30, Appli
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US-09-885-453-1	US-09-943-798-4	US-10-400-991-6	`US-10-167-192-3	-10-692	-10	-10-349-021-		US-10-055-106C-3	US-09-991-225-6	US-09-779-679-27	US-09-828-478-5	9-866-230-	US-10-290-078-21	US-10-296-115-1356	US-10-775-965-110	10-369-405-	US-09-991-225-2	0	US-10-369-405-55			-10	-10-321-807-	US-10-757-262-40	-10 - 314	Ļ	0-297	US-10-343-650A-58	-10-403-161-2	-10-403-161-	US-10-182-605-2
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ALIGNMENTS

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APPLICANT: Pfizer Inc
TITLE OF INVENTION: No. US20010039037Aiel Polypeptide
FILE REFERENCE: PC10914ADAM
CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR PILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR PILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NO 6
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US-09-826-791-6
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                                                                                                                                                                                                                                                                                                                          LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
121 NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                              61 YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
                                                                                                       61 YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
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US-09-866-230-7
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Sequence 9, Application US/09866230
PATENT NO. US20020150901A1
GENERAL INFORMATION:
APPLICANT: Murphy, Andrew, et al.
TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
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APPLICANT: Murphy, Andrew, et al.
APPLICANT: Murphy, Andrew, et al.
TITLE OF INVENTION: NO. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
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Best Local Similarity
Matches 346; Conserv
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 3e-148;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/828,47
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.
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                                                                                                                                                                                                               ; ORGANISM: Homo US-09-828-478-2
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US-09-828-478-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation
TITLE OF INVENTION: Protein
FILE REFERENCE: 04974.00458
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/207,
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
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ORGANISM: Homo
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                                                            MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
                                                                                    MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
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                                                                                                                                   Score 1788; DB 9
Pred. No. 3e-148;
); Mismatches 0
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US-09-779-679-2
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                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-679-2
                            Query Match
Best Local Similarity
Matches 346; Conserv
                                                                                                                                                                   SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09779679 Publication No. US20030082757A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/183191
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/180,929
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
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APPLICANT: Mezes, Peter S
TITLE OF INVENTION: NO. US20030082757A1el Proteins and Nucleic Acids
FILE REFERENCE: 15966-661
CURRENT APPLICATION NUMBER: US/09/779,679
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APPLICANT: Burgess, Catherine
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                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USSN 60/181392 FILING DATE: 2000-02-09
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                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN 60/221341
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FILING DATE: 2000-02-09
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Padigaru, Muralidhara
Tchernev, Velizar T
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Casman, Stacie
Ballinger, Robert
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                                 Conservative
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Pred. No. 3
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RESULT 6
US-09-779-679-26
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PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/183191.
PRIOR APPLICATION NUMBER: USSN 60/180,929
PRIOR FILING DATE: 2000-02-08
PRIOR PILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/219758
PRIOR APPLICATION NUMBER: USSN 60/181339
PRIOR APPLICATION NUMBER: USSN 60/181349
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR APPLICATION NUMBER: USSN 60/181341
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR APPLICATION NUMBER: USSN 60/21341
PRIOR APPLICATION NUMBER: USSN 60/181392
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
                                              SOFTWARE: Pa
SEQ ID NO 26
LENGTH: 346
TYPE: PRT
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ORGANISM: Homo sapiens
                                                                                                                                                                      PRIOR APPLICATION NUMBER: USSN 60/219585
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181157
PRIOR FILING DATE: 2000-02-09
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APPLICANT: Burgess, Catheri
APPLICANT: Padigaru, Murali
APPLICANT: Tchernev, Veliza
APPLICANT: Mishra, Vishnu S
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TITLE OF INVENTION: No. US20030082757A1el Proteins
FILE REFERENCE: 15966-661
                                                                                                                               NUMBER OF SEQ ID NOS: 65
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                                                                      346
                                                                                                                       PatentIn Ver.
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Casman, Stacie
Ballinger, Robert
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Tchernev, Velizar T
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; ORGANISM: Homo sapiens
US-09-991-225-30
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US-09-991-225-30
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Publication No. US20030153063A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
FILE REFERENCE: D0075, NP
CURRENT APPLICATION NUMBER: US/09/91,225
CURRENT PILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR APPLICATION NUMBER: 60/257,611
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Best Local Simi
Matches 346;
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                                                                          NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ 180
                                                                                                  NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 5628963CD1
US-09-980-049-1
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US-09-980-049-1
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Best Local Similarity 100.0%;
Matches 346; Conservative 0
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BAUGHN, Mariah R.
GRAUL, Richard
KHAN, Farrah A.
NGUYEN, Danniel B.
PATTERSON, Chandra
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HAFALIA, April
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AU-YOUNG, Janice
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APPLICANT: WALLA, Natinder K.
APPLICANT: DAS, Debopriya
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0072 PCT
CURRENT APPLICATION NUMBER: US/09/980,049
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
PRIOR PRILING DATE: 2000-03-29; 2000-04-06; 2000-04-20; 2000-04-28; 2000-05-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 346
TYPE: PRT
ORGANISM: Homo mapiens
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SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
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Pred. No. 3e-148;
0; Mismatches 0; Indels 0;
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; ORGANISM: Homo sapiens
US-10-225-567A-589
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CURRENT APPLICATION NUMBER: US/10/349,021
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10349021 Publication No. US20030157541A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 589
LENGTH: 346
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Best Local
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                                                                                                                                                                                                                            APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like
TITLE OF INVENTION: Protein
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/09/714,008
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR PILING DATE: 1999-11-17
PRIOR PILING DATE: 1999-11-17
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PRIOR PILING DATE: 1999-11-17
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US-10-321-807-14
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                                                                                      PRIOR APPLICATION NUMBER: 60/171,902
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/171,901
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/171,900
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR FILING DATE: 2000-02-11
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SEQ ID NO 2
LENGTH: 346
TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 3e
Matches 346; Conservative 0; Mismatches
                        Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 133 SOPTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Rupong
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: No. US20030166148A1-Endogenous,
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ARENOO86
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Constitutively Activated Human

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240

Wrapper or

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Sequence 2, Application US/10131332A

Publication No. US20030203833A1

GENERAL INFORMATION:

APPLICANT: Ignar, Diane
APPLICANT: Pillai, Sreekumar

ITILE OF INVENTION: Cysteine Leukotriene 2 Receptor Pol
FILE REFERENCE: PU4824

CURRENT APPLICATION NUMBER: US/10/131,332A

CURRENT FILING DATE: 2002-07-02

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 346

TYPE: PRT

ORGANISM: Homo sapiens

US-10-131-332A-2
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; TYPE: PRT
; ORGANISM: Homo s
US-10-321-807-14
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Matches 346
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Similarity 100.0%;
                                                      NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ 180
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Pred. No. 3e-148;
Mismatches (
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Pred. No. 3e-148;
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP
TITLE OF INVENTION: THEREOF
FILE REFERENCE: DO075A CIP
CURRENT APPLICATION NUMBER: US/10/369,405
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: U.S. 60/249,613
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: U.S. 09/991,225
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: U.S. 60/257,611
PRIOR APPLICATION NUMBER: U.S. 60/257,611
PRIOR APPLICATION NUMBER: U.S. 60/305,818
PRIOR APPLICATION NUMBER: U.S. 60/305,818
PRIOR APPLICATION NUMBER: U.S. 60/305,818
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US-10-369-405-30
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SOFTWARE: PatentIn version
SEQ ID NO 30
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1788; DB 14; Best Local Similarity 100.0%; Pred. No. 3e-148;
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ORGANISM: Homo sapiens
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NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV
                                                                                     SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKORLHKALVITLALAAANACF
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                                                                     SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
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RESULT 14
US-10-182-605-2
; Sequence 2, Application US/10182605
; Publication No. US20040023861A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL PROTEIN
; FILE REFERENCE: N78955A

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RESULT 15
US-10-403-161-22
J Sequence 22, Application US/10403161
Publication No. US20040043930A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/370349
PRIOR FILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: 60/370969
PRIOR PILING DATE: 2002-04-08
PRIOR PILING DATE: 2002-08-15
PRIOR PILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/372019
PRIOR PILING DATE: 2002-04-12
PRIOR PILING DATE: 2002-04-22
PRIOR PILING DATE: 2002-04-22
PRIOR PILING DATE: 2002-04-09/779679
PRIOR PILING DATE: 2002-09-09/779679
PRIOR APPLICATION NUMBER: 60/181045
PRIOR APPLICATION NUMBER: 60/181045
PRIOR PILING DATE: 2000-02-08
PRIOR PILING DATE: 2000-02-08
PRIOR PILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/65897
PRIOR APPLICATION NUMBER: 60/66892
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-605-2
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Best Local Similarity 100.0%;
Matches 346; Conservative C
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CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: GB 0003079.1
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 21402-573C
CURRENT APPLICATION NUMBER: US/10/403,161
CURRENT FILING DATE: 2003-03-31
CURRENT FILING DATE: 2003-03-31
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Pred. No. 3e-148;
                                            See File Wrapper
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US-10-403-161-22
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SEQ ID NO 22
LENGTH: 346
TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0
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 NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                       SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
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Search completed: December 13, 2004, 18:05:05 Job time: 149 secs THIS PAGE BLANK (USPro)

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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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356.5	356.5	357	357	359	360	361.5	362.5	363	366	366.5	367.5	371.5	372	372.5	373.5
19.9	19.9	20.0	20.0	20.1	20.1	20.2	20.3	20.3	20.5	20.5	20.6	20.8	20.8	20.8	20.9
361	333	363	328	363	432	352	369	359	362	355	427	365	363	378	387
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	2
JC5653	165989	A49092	JC4800	148261	A43448	A43113	JC2083	S15403	JN0694	G02436	S17148	S68208	I57940	A55735	169202
G protein-coupled	G protein-coupled	angiotensin II rec	P2Y6 receptor - hu	angiotensin II rec	thrombin receptor	chemokine (C-C) re	somatostatin recep	angiotensin II rec	angiotensin II rec	chemokine (C-C) re	alpha-thrombin rec	G protein-coupled	somatostatin recep	G protein-coupled	G protein-coupled

ALIGNMENTS

G protein-coupled receptor - chicken C;Species: Gallus gallus (chicken) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004 C;Accession: S33733 R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; PEBS Lett. 324, 219-225, 1993

Burnsto

FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor. A;Reference number: 833733; MUID:93285340; PMID:8508924
A;Accession: \$33733

A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-362 < WEB>
A;Residues: 1-362 < WEB>
C;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395
C;Superfamily: ATP receptor P2u

C;Superfamily: ATP receptor P2u C;Keywords: G protein-coupled receptor; transmembrane protein

Length 362;

Query Match

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heptahelical P2Y5-like receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                    195 TADEYLRSYFVYSMCTTVFMFCI-----PFIVILGCYGLIVKALIYKDLDNSPLR---RK
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                                                                                                                                                                                                                                                                                                                                                                                         134 VVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                  76 SYYMFNLALADFLYYLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                    CFNPLLYYFAGENFKDRLKSALRK 322
                                                                                                                                                                                                             SIYLVIIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNS
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                                                                                                                                                                                                                                                                                                                  -----LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRK 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Score 470; DB 2; 30.6%; Pred. No. 6.1e-31;
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RESULT 3

150241

Grotein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 0
C;Accession: 150241; JC4618
C;Accession: 150241; JC4618
A;Taltle: Identification of a G protein coupled receptor induced in A;Reference number: 150241; MUID:93329058; PMID:8393036
A;Reference number: 150241; MUID:93329058; PMID:8393036
A;Recession: 150241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <KAP>
A;Residues: 1-308 <KAP>
A;Residues: 1-308 <KAP>
A;Reference number: JC4618; MUID:931250; GB:L06109; NID:9304383; PIDN:A;Residues: 1-308 <KAP>
A;Residues: 1-308 <KAP>
A;Residues: 1-308 <KAP>
A;Residues: 1-308 <MEB>
A;Accession: JC4618; MUID:9619677; PMID:8619790
A;Recession: JC4618; MUID:9619677; PMID:8619790
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:9304383; PIDN:AAB06587.1; PID:A;Experimental source: T-cells
C;Gomment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM2>
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R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D. Biochem. Biochys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely A;Reference number: JC5549; MUID:97366605; PMID:923435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 «JAN»
A;Residues: 1-370 «JAN»
A;Cossiones: UNIPROT:099677; DDBJ:AF005419; NID:922C;Superfamily: ATP receptor P2u
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Alternate names: purinoceptor 6H1
Saltus gallus (chicken)
Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
Accession: I50241; JC4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Pred. No. 4.2e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAB06587.1;
                                                                                                                                                                                                                                  PID: 9304384
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R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P. Biochem. Biophys. Res. Commun. 218, 798-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor. A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615; MUID:96158962; PMID:8579591
A;Residues: 1-373 <AYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: erythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Bescription: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Status: rraisaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor P2Y1 - human

N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence revision 16-Aug-1996 #text_change 09-Jul-
C;Accession: JC4737; JC4615; \(\overline{S}\)4253

R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.;

Biochem. Biophys. Res. Commun. 221; 588-593; 1996

A;Title: Cloning and tissue distribution of the human P2Y1 receptor.

A;Reference number: JC4737; MUID:96205320; PMID:8630005

A;Accession: JC4737; MUID:96205320; PMID:8630005
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
P;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:Z49205;
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                                                                                                                                                                                                      C; Comment: This
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A; Residues: 1-373 < JAN>
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                                                                                                                                                     A;Gene: p2Y1; GDB:P2RY1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRNCTIE-NEKREFEPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQNNTEQRTCFE-NFPESTWKTYLSR 180
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Pred. No. 3.9e-29;
3; Mismatches 119;
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RESULT 5

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P2Y receptor - bovine
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R.Henderson, D.G.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Da...
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F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLIIFFLCFLPYHTLRTVHLTT----WKVGLC--KDRLHKALVITLALAAANACFNPLL 304
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Pred. No. 5.7e-29;
9; Mismatches 111
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A;Rote: sequence extracted from NCBI backbone (NCBIN:127096, C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: B45680
R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, J. Virol. 67, 209-2220, 1993
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific A;Reference number: A45680; MUID:93188173; PMID:8383238
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A;Molecule type: nucleic acid
A;Residues: 1-361 <BIR>
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32.1%; Pred. No. 1.7e-28,
tive 63; Mismatches 139
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PIDN:AAA35924.1; PID:g29205

protein-coupled

NCBIP: 127097)

18;

Gaps

78

304

248

251 191 196 131 138 71

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intron 17 purinergic receptor P2Y5 - human
N;Alternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the
A;Reference number: Z16705
A;Accession: T09508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRVA
A;Residues: 1-344 <BOH>
A;Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:g2232068; PID:g2232069
C;Genetics:
A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                     RESULT 8

A47556

ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-0;C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-0;C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblast A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Recession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS
A;Cross-references: UNIPROT:P35383; GB:L14751; NID:g309457; PIDN:AAJ
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein
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Matches 106
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| NGTFSNNN-SRNCTI-ENFKREFFFIVYLIIFFWGVLGNGLSIYVFLQPY
                                                                                 23.6%;
                                                            69;
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Pred. No. 3.4e-28;
                                                                                 Score 421.5;
Pred. No. 5.6
                                                          Mismatches
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                                                                                 .6e-27;
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                                                                                                  DB 2;
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                                                                                                                                                                             PIDN:AAA39871.1; PID:g30945
                                                            29;
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RESULT A54946 P-2U nu

nucleotide 10

receptor

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A;Title: Cloning by functional expression of platelet-activating factor receptor A;Reference number: $13638; MUID:91101726; PMID:1846231 A;Accession: $13638 A;Residues: preliminary A;Molecule type: mRNA A;Residues: 1-342 <HON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                platelet-activating factor receptor - guinea pig (;Speciaes: Cavia porcellus (guinea pig) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 C;Accession: S13638 R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Wa
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                                                                                                                                                                                                                                                                          RLLHVTSIRSAWILCGIIWILIM--ASSIMLLD-----SGSEQNGSVTSCLELNLYKIAK 197
                                    DRLKSALRKGHPQKAKTKC
                                                                                                              LCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPLLYYFAGENFK 313
                                                                                                                                                                                            LOTMNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF
                                                                                                                                                                                                                                     KTAQATTRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNKAGSGNITRCFE-HYEKGSK
                                                                                                                                                                                                                                                                                                                 LLFLITLPLWIVYYSNQGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPI
                                                                                                                                                                                                                                                                                                                                     LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF
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                                                                         ICFVPHHMVQ-LPWTLAELGMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFR
                                                                                                                                                     PVLIIHICIVLGFFIVFLLILFCNLVIIHTLLRQPVKQQRNAEVRRALWMVCTVLAVFV
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-NIMRSSQKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 416; DB 2;
Pred. No. 1.4e-26;
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R; Fart, C.B.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J. Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994

A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cysti A; Reference number: A54946; MUID:94211846; PMID:8159738

A; Accession: A54946

A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 1-375 <-APR>
A; Cross-references: GB:U07225

A; Note: parts of this sequence were confirmed by protein sequencing
C; Genetics:
A; Gene: GDB:P2RY2; HP2U; P2U
A; Cross-references: GDB:362713; OMIM:600041
C; Supprfamily: ATP receptor P2u
C; Keywords: G protein-complex
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                                                                                                                                            A;Cross-references: UNIDROT: P25105; GB: W76674; NID: 9456293; R;Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G. Blochem. Biophys. Res. Commun. 180, 105-111, 1991
A;Title: Characterization of a human cDNA that encodes a fun. A;Reference number: JH0479; MUID: 92028922; PMID: 1656963
A;Accession: JH0479
A;Molecule type: mRNA
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A40191
platelet-activating factor receptor -
platelet-activating factor receptor -
C;Species: Homo saplens (man)
C;Date: 28-Aug-1992 #sequence revision
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C;Date:
C;Access
R;Parr,
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A; Residues: 1-342 < KUN>
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;Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1;
;Experimental source: granulocyte, cell line HL-60 all
;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.
                                                                                                                 ;Molecule type: mRNA
;Residues: 1-342 <YER>
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;Date: 11-Nov-:
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11-Nov-1994 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK 197
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                                                                        PID:g189538
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       Bito,
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A;Note: the authors translated the codon AAT for residue 316 R;Seyfried, C.B.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992
A;Title: The human platelet-activating factor receptor gene (A;Reference number: A42831; MUID:92347886; PMID:1322356
A;Accession: A42831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-226,'TG',229-342 <SEY>
A;Residues: 1-226,'TG',229-342 <SEY>
A;Residues: 1-226,'TG',229-342 <SEY>
A;Residues: 1-226,'TG',229-342 <SEY>
A;Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698
A;Onte: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
A;Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for A;Reference number: IS1923; MUID:93192035; PMID:8383507
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A;Title: Molecular cloning and expression of platelet-activating A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079
A;Status: not compared with conceptual translation
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C;Superfamily: ATP receptor P2u
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A;Molecule type: DNA
A;Residues: 1-342 <RES>
A;Cross-references: GB:S56396; NID:g298580; PIDN:AAI
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A; Residues: 1-315,'N',317-342 < SUG:
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A; Residues: 1-342 < NAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: heart
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Best Local
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                                                                                                                                                      188
                                                                                                                                                                                                   114 NRFQAVTRPIKTAQANTRKRGISLSLVIWVAIVGAASYFLILDSTNTVPDSAGSGNVTRC
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MVCTVLAVFIICFVPHHVVQ-LPWTLAELGFQDSKFHQAINDAHQVTLCLLSTNCVLDPV
                                               TIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPL
                                                                                                                                      LBLNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVBVPBSGLRVSHRKALT
                                                                                                                                                                                                                                                   VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDS-----GSEQNGSVTSC
                                                                                                                                                                                                                                                                                                VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 134
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                                                                                               FE-HYEKGSVPVLIIHIFIVFSFFLVFLIILFCNLVIIRTLLMQPVQQQRNAEVKRRALW
                                                                                                                                                                                                                                                                                                                                                                                                         MEPHDS-SHMDS-----EFRYTLFPIVYSIIFVLGVIANGYVLWVFARLYPCKKFNEIK
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#status predicted <TRV>
#status predicted <TVI>
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C;Species: Xenopus laevis (C;Species: 13-Sep-1996 #sequen C;Accession: 151667 R;Gerszten, R.E.; Chen, J.; Nature 368, 648-651, 1994
                                                                                                                    platelet activating factor receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S63666
R;Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimi
Biochem. J. 314, 671-678, 1996
A;Title: A murine platelet-activating factor receptor gene: cloning, chromose
A;Reference number: S63666; MUID:96239129; PMID:8670084
A;Accession: S63666
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-341 <ISH>
A;Rosesidues: UNLPROT:062035; EMBL:D50872; NID:g1256924; PIDN:BAA09468
C;Superfamily: ATP receptor P2u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I51667
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                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
MEPNGTFSNNNSRNCTIENFKREFFFIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN
                                                                                                                                                                                                                                                                                                                                                                                                                               ACVGSVSCCLDPLIYYYASSQCQRYLYSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTQKIPRLDITTCHDVLDLKDLKDFYIYYFSSF--CLLFFFVPFIITTICYIGIIRSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYCNMYCSVLLIASISVDRFLAVVYPMHSLSWRTMSRAYMACSFIWLISIASTIPLLVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSIENS----CKKTRALFLAVVVLCVFIICFGPTNVLFLTHY----LQEANEFLYFAYILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEVPESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ---NGSVTSCLELNLYKIAKLQTMNYIALVVGCLL----PFFTLSICYLLIIRVLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAIIIFLFKMKVRKPAVVYMLNLAIADVFFVSVLPFKIAYHLSGNDWLFGPGMCRIVTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSIYVELQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEPNGTFSNNNS------RNCTIE-----NFKREFFPIVYLIIFFWGVLGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYYFAGENFKDRLKSALRKGHPQKAKTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LALAAANACFNPLLYYFAGENFKDRLKSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELDESGEGSGDQAPVSRSARKPIRRNITKEAEQYLSSQWLTKFVPSLYTVVFIVGLPLNL
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen, J.; Ishii, M.; Ishii, K.;
                                                                    22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.7%;
30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KHLTEKFYSMRSSRKC
                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66;
                                                   Score 404; DB 2; I
Pred. No. 1.4e-25;
6; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 406; DB 2;
Pred. No. 1.2e-25;
6; Mismatches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
                                                                                                                                     EMBL:D50872; NID:g1256924; PIDN:BAA09468.1;
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                                                                                 Length 341,
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                                                    Indels
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                                                                                                                                                                                                                                                                      T.; Shimizu,
                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                     74
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                                                                                                                                     PID:g12
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A; Introns: 28/1
C; Superfamily: A;
F; 1-36/Domain: ac
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                                 문
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A; Residues: 1-397 < NYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S66518
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Title: Molecular cloning and functional expression of A, Reference number: S66518; MUID:96048032; PMID:7556175
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Best Local
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4
                                                                                                    99;
                                                                                                                      Similarity
   RGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVIYCFLTKKFRKHLS---EKFYSMRSSRKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLYYFAGENFKDRLKSALRKGHPQKAKTKC
                                                                                                    Conservative
                                                                                                                  22.4%;
                                                                                                      69;
                                                                                                    Score 400.5; DB 2
Pred. No. 3.1e-25;
9; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316
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                                                                                                                                  DB 2;
                                                                                                    121;
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A;Molecule type: mRNA
A;Residues: 1-137, A;139-397 <BOE>
A;Residues: 1-137, A;139-397 <BOE>
A;Residues: 1-137, A;139-397 <BOE>
A;Rose-ferences: EMBL.U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
A;Note: the authors translated the codon GTC for residue 68 as Ile and AAC fc
R;Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A;Reference number: H00822
A;Reference number: H00822
A;Reference number: H00822
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Biochem. J. 314, 109-1016, 1996
A;Title: Molecular cloning, expression and potential functions of the human proteinase-a A;Reference number: S64709; MUID:96177879; PMID:8615752
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(;Species: Homo sapiens (man)
(;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Ju:
C;Accession: $66518; $64709; $602131
C;Accession: $66518; $64709; $602131
R;Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Sundelin,
Bur. J. Biochem. 232, 84-89, 1995
                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: ATP receptor P2u
F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 134
                                                                                                        FFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYL 99
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FLPIVYTIVFVVGLPSNGMALWVFLFRTKKKHPAVIYMANLALADLLSVIWFPLKIAYHI
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                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                         397;
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159

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angiotensin receptor homolog APJ - human C;Species: Homo sapiens (man) c;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004 C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004 C;Accession: 138435 R;O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr Gene 136, 355-360, 1993 Gene 136, 355-360, 1993 A;Title: A human gene that shows identity with the gene encoding the angiotensin recepto A;Reference number: 138435; MUID:94124031; PMID:8294032 A;Accession: 138435
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Search completed: December 13, 2004, 17:53:20 Job time : 42 secs
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A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
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;Residues: 1-380 KRS>
;Cross-references: UNIPROT:P35414; EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.3%; Score 398; DB 2; Length 380; Best Local Similarity 29.2%; Pred. No. 4.7e-25; Matches 100; Conservative 71; Mismatches 134; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                        290
                                                                                                                                                                     239 ---GLR-KRRRLLSIIVVLVVTFALCMMPYHLVKTLYMLGSLLHWP----CDFDLFLMNIF 291
                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                       181 CY-MDYSMVATVSSEWAWEVGLGVSSTTVGFVVPFTIMLTCYFFIAQTIAGHFRKERIE-
                                                                                                                                                                                                                                                                                                    187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AĻVVĢC-ĻLPFFTLSICYLĻIIRVĻLKVEVPESGLRVSHRKALTTIIITĻIIFFLÇFLPY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 - CRSVRTVKQMQVSLTSKKHSR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 HPQKAKTKCVFPVSVWLRKETR 345
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                                                                                                                                                                                                                                                                                                                                                                                                                              61 RRSADIFIASLAVADLTEVVTLPLWATYTYRDYDWPFGTFFCKLSSYLIFVNNYASVFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 MEPNGTFSN----NNSRNCTIENFKRE--FFPIVYLIIFFWGVLGNGLSIY-VFLQPYKK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 STSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 129
                                                                                                                        --TLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKT 330
                                                                                                                                                                                                              PESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVH----LTTWKVGLCKDRLHKALVI 289
                                                                                                                                                                                                                                                                                                  CLELNLYKIAKLQT------MNYIALVVGCLLPFFTLSICYLLIIRVLL------KVEV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYCTCISYVNSCLNPFLYAFFDPRFRQACTSMLCCGQSRCAGT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEEGGDFDNYYGADNQSECEYTDWKSSGALIPAIYMLVFLLGTTGNGLVLWTVFRSSREK 60
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